Resource Summary Report

Generated by FDI Lab - SciCrunch.org on Mar 31, 2025

Animal QTLdb

RRID:SCR_001748
Type: Tool

Proper Citation

Animal QTLdb (RRID:SCR_001748)

Resource Information

URL: http://www.animalgenome.org/cgi-bin/QTLdb/index

Proper Citation: Animal QTLdb (RRID:SCR_001748)

Description: Database of trait mapping data, i.e. QTL (phenotype / expression, eQTL), candidate gene and association data (GWAS) and copy number variations (CNV) mapped to livestock animal genomes, to facilitate locating and comparing discoveries within and between species. New data and database tools are continually developed to align various trait mapping data to map-based genome features, such as annotated genes. QTLdb is open to house QTL/association date from other animal species where feasible. Most scientific journals require that any original QTL/association data be deposited into public databases before paper may be accepted for publication. User curator accounts are provided for direct data deposit. Users can download QTLdb data from each species or individual chromosome.

Abbreviations: Animal QTLdb

Synonyms: Animal QTL database, Animal Quantitative Trait Loci database, AnimalQTLdb, Animal Quantitative Trait Loci (QTL) database

Resource Type: database, data repository, data or information resource, storage service resource, service resource

Defining Citation: PMID:23180796, PMID:17245610

Keywords: chromosome, comparative genomics, dna sequence, genome, livestock, quantitative trait locus, non-human animal, structural genomics, single-nucleotide polymorphism, gene association, genomics, trait, copy number variation, trait, phenotype, expression, eqtl, genome wide association study, candidate gene, genotype

Funding: USDA NRSP-8;

USDA 2007-04187

Availability: Free, Freely available

Resource Name: Animal QTLdb

Resource ID: SCR_001748

Alternate IDs: nif-0000-02550

Alternate URLs: http://www.animalgenome.org/QTLdb/

Record Creation Time: 20220129T080209+0000

Record Last Update: 20250331T060122+0000

Ratings and Alerts

No rating or validation information has been found for Animal QTLdb.

No alerts have been found for Animal QTLdb.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 48 mentions in open access literature.

Listed below are recent publications. The full list is available at FDI Lab - SciCrunch.org.

Xing Y, et al. (2024) The role of RNA epigenetic modification-related genes in the immune response of cattle to mastitis induced by Staphylococcus aureus. Animal bioscience, 37(7), 1141.

Beiki H, et al. (2024) Enhanced bovine genome annotation through integration of transcriptomics and epi-transcriptomics datasets facilitates genomic biology. GigaScience, 13.

Liu J, et al. (2023) Genome-Wide Association Analysis of Reproductive Traits in Chinese Holstein Cattle. Genes, 15(1).

Zhang M, et al. (2023) Managing genomic diversity in conservation programs of Chinese domestic chickens. Genetics, selection, evolution : GSE, 55(1), 92.

Argyriadou A, et al. (2023) A genome-wide association study reveals novel SNP markers

associated with resilience traits in two Mediterranean dairy sheep breeds. Frontiers in genetics, 14, 1294573.

Wang H, et al. (2022) Genome-Wide Association Study of Growth Traits in a Four-Way Crossbred Pig Population. Genes, 13(11).

Cao X, et al. (2021) Comparative Enhancer Map of Cattle Muscle Genome Annotated by ATAC-Seq. Frontiers in veterinary science, 8, 782409.

Kou M, et al. (2020) Expression pattern and association analysis of porcine matrix metallopeptidase 9 (MMP9) with diarrhea and performance traits in piglets. Research in veterinary science, 129, 53.

Purfield DC, et al. (2020) Breed- and trait-specific associations define the genetic architecture of calving performance traits in cattle. Journal of animal science, 98(5).

Zinovieva NA, et al. (2020) Selection signatures in two oldest Russian native cattle breeds revealed using high-density single nucleotide polymorphism analysis. PloS one, 15(11), e0242200.

Czech B, et al. (2020) Patterns of DNA variation between the autosomes, the X chromosome and the Y chromosome in Bos taurus genome. Scientific reports, 10(1), 13641.

Alshawi A, et al. (2019) Genome Analysis Reveals Genetic Admixture and Signature of Selection for Productivity and Environmental Traits in Iraqi Cattle. Frontiers in genetics, 10, 609.

Han B, et al. (2019) Identification of single nucleotide polymorphisms of PIK3R1 and DUSP1 genes and their genetic associations with milk production traits in dairy cows. Journal of animal science and biotechnology, 10, 81.

Kommadath A, et al. (2019) A large interactive visual database of copy number variants discovered in taurine cattle. GigaScience, 8(6).

Liu M, et al. (2019) Array CGH-based detection of CNV regions and their potential association with reproduction and other economic traits in Holsteins. BMC genomics, 20(1), 181.

Jiang J, et al. (2019) Determination of genetic associations between indels in 11 candidate genes and milk composition traits in Chinese Holstein population. BMC genetics, 20(1), 48.

Alexandre PA, et al. (2019) Systems Biology Reveals NR2F6 and TGFB1 as Key Regulators of Feed Efficiency in Beef Cattle. Frontiers in genetics, 10, 230.

Purfield DC, et al. (2019) Reaffirmation of known major genes and the identification of novel candidate genes associated with carcass-related metrics based on whole genome sequence within a large multi-breed cattle population. BMC genomics, 20(1), 720.

Purfield DC, et al. (2019) Genomic Regions Associated With Gestation Length Detected

Using Whole-Genome Sequence Data Differ Between Dairy and Beef Cattle. Frontiers in genetics, 10, 1068.

Gao Y, et al. (2018) Genome-wide association study of Mycobacterium avium subspecies Paratuberculosis infection in Chinese Holstein. BMC genomics, 19(1), 972.